

SEQUENCE LISTING

<110> FUJIWARA, TSUTOMU
WATANABE, TAKESHI
HORIE, MASATO

<120> AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

<130> Q-53599

<140> 09/273,565

<141> 1999-03-22

<150> 09/055,699

<151> 1998-04-07

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<151> 1997-03-19

<150> JP 63410/1996

<151> 1996-03-19

<150> JP 69163/1997

<151> 1997-03-05

<160> 95

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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35 40 45

Pro Gly Glu Arg Glu Leu Thr Ile Pro Ala Ser Ala Asn Val Phe Tyr
50 55 60

Pro Met Asp Gly Ala Ser His Asp Phe Leu Leu Arg Gln Arg Arg Arg
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Ser Ser Thr Ala Thr Pro Gly Val Thr Ser Gly Pro Ser Ala Ser Gly
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Thr Gly Arg Lys Ile Ala Arg Ala Leu Phe
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Tyr Lys Ser Ile Leu Val Thr Ser Gln Asp Lys Ala Pro Ser Val Ile
10 15 20 25
agt cgt gtc ctt aag aaa aac aat cgt gac tct gca gtg gct tca gag 150
Ser Arg Val Leu Lys Lys Asn Asn Arg Asp Ser Ala Val Ala Ser Glu
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tat gag ctg gta cag ctg cta cca ggg gag cga gag ctg act atc cca 198
Tyr Glu Leu Val Gln Leu Leu Pro Gly Glu Arg Glu Leu Thr Ile Pro
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gcc tcg gct aat gta ttc tac ccc atg gat gga gct tca cac gat ttc 246
Ala Ser Ala Asn Val Phe Tyr Pro Met Asp Gly Ala Ser His Asp Phe
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ctc ctg cgg cag cgg cga agg tcc tct act gct aca cct ggc gtc acc 294
Leu Leu Arg Gln Arg Arg Arg Ser Ser Thr Ala Thr Pro Gly Val Thr
75 80 85

agt ggc ccg tct gcc tca gga act cct ccg agt gag gga gga ggg ggc 342
 Ser Gly Pro Ser Ala Ser Gly Thr Pro Pro Ser Glu Gly Gly Gly Gly
 90 95 100 105

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 Ser Phe Pro Arg Ile Lys Ala Thr Gly Arg Lys Ile Ala Arg Ala Leu
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Asp Val Ser Arg Val Glu Lys Tyr Thr Ile Ser Gln Glu Ala Tyr Asp
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Gln Arg Gln Asp Thr Val Arg Ser Phe Leu Lys Arg Ser Lys Leu Gly
 65 70 75 80

Arg Tyr Asn Glu Glu Glu Arg Ala Gln Gln Glu Ala Glu Ala Ala Gln
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Arg Leu Ala Glu Glu Lys Ala Gln Ala Ser Ser Ile Pro Val Gly Ser
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Arg Cys Glu Val Arg Ala Ala Gly Gln Ser Pro Arg Arg Gly Thr Val
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Met Tyr Val Gly Leu Thr Asp Phe Lys Pro Gly Tyr Trp Ile Gly Val
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Arg Tyr Asp Glu Pro Leu Gly Lys Asn Asp Gly Ser Val Asn Gly Lys
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 gatggaggtg acgggggtgt cggcaccacg gtgaccgttt tcatcagcag ctccctcagc 180
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 35 40 45
 Gly Ile Ser Glu Phe Ile Val Met Ala Ala Asp Ala Glu Pro Leu Glu
 50 55 60
 Ile Ile Leu His Leu Pro Leu Leu Cys Glu Asp Lys Asn Val Pro Tyr
 65 70 75 80
 Val Phe Val Arg Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly Val Ser
 85 90 95
 Arg Pro Val Ile Ala Cys Ser Val Thr Ile Lys Glu Gly Ser Gln Leu
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 Lys Gln Gln Ile Gln Ser Ile Gln Gln Ser Ile Glu Arg Leu Leu Val
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 Met Thr Glu Ala Asp Val Asn
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cca aag gcc tat ccc ctt gcc gat gcc cac ctc acc aag aag cta ctg 163
 Pro Lys Ala Tyr Pro Leu Ala Asp Ala His Leu Thr Lys Lys Leu Leu
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gac ctc gtt cag cag tca tgt aac tat aag cag ctt cgg aaa gga gcc 211
 Asp Leu Val Gln Gln Ser Cys Asn Tyr Lys Gln Leu Arg Lys Gly Ala
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atg gct gca gac gcc gag cca ctg gag atc att ctg cac ctg ccg ctg 307
 Met Ala Ala Asp Ala Glu Pro Leu Glu Ile Ile Leu His Leu Pro Leu
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 Ala Leu Gly Arg Ala Cys Gly Val Ser Arg Pro Val Ile Ala Cys Ser
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 Val Thr Ile Lys Glu Gly Ser Gln Leu Lys Gln Gln Ile Gln Ser Ile
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 Gln Gln Ser Ile Glu Arg Leu Leu Val
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 35 40 45

Arg Cys Leu Tyr Arg Asp Val Met Leu Glu Leu Tyr Ser His Leu Phe
 50 55 60

Ala Val Gly Tyr His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu
 65 70 75 80

Lys Glu Lys Glu Pro Arg Val Glu Glu Ala Glu Val Ser His Gln Arg
 85 90 95

Cys Gln Glu Arg Glu Phe Gly Leu Glu Ile Pro Gln Lys Glu Ile Ser
 100 105 110

Lys Lys Ala Ser Phe Gln Lys Asp Met Val Gly Glu Phe Thr Arg Asp
 115 120 125

Gly Ser Trp Cys Ser Ile Leu Glu Glu Leu Arg Leu Asp Ala Asp Arg
 130 135 140

Thr Lys Lys Asp Glu Gln Asn Gln Ile Gln Pro Met Ser His Ser Ala
 145 150 155 160

Phe Phe Asn Lys Lys Thr Leu Asn Thr Glu Ser Asn Cys Glu Tyr Lys
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Asp Pro Gly Lys Met Ile Arg Thr Arg Pro His Leu Ala Ser Ser Gln
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 Lys Gln Pro Gln Lys Cys Cys Leu Phe Thr Glu Ser Leu Lys Leu Asn
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 Asp Val Val Gly Ser Gly Gln Leu Phe Ser His Ser Ser Ser Asp Ala
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 Cys Ser Lys Asn Ile His Thr Gly Glu Thr Phe Cys Lys Gly Asn Gln
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 Cys Arg Lys Val Cys Gly His Lys Gln Ser Leu Lys Gln His Gln Ile
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 His Thr Gln Lys Lys Pro Asp Gly Cys Ser Glu Cys Gly Gly Ser Phe
 275 280 285
 Thr Gln Lys Ser His Leu Phe Ala Gln Gln Arg Ile His Ser Val Gly
 290 295 300
 Asn Leu His Glu Cys Gly Lys Cys Gly Lys Ala Phe Met Pro Gln Leu
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 325 330 335
 Cys Lys Glu Cys Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr
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 His Gln Lys Thr His Thr Arg Lys Lys Pro Tyr Lys Cys His Asp Cys
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 Gly Lys Ala Phe Phe Gln Met Leu Ser Leu Phe Arg His Gln Arg Thr
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 His Ser Arg Glu Lys Leu Tyr Glu Cys Ser Glu Cys Gly Lys Gly Phe
 385 390 395 400
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 Thr Leu Ser Leu His Gln Arg Ile His Ser Gly Gln Lys Ser Tyr Val
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 Cys Ile Glu Cys Gly Gln Ala Phe Ile Gln Lys Ala His Leu Ile Val
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 His Gln Arg Ser His Thr Gly Glu Lys Pro Tyr Gln Cys His Asn Cys
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 Gly Lys Ala Phe Asn Gly Arg Ser Asn Phe His Lys His Gln Ile Thr
 595 600 605
 His Thr Arg Glu Arg Pro Phe Val Cys Tyr Lys Cys Gly Lys Ala Phe
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 Val Gln Lys Ser Glu Leu Ile Thr His Gln Arg Thr His Met Gly Glu
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 Lys Pro Tyr Glu Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro
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 660 665 670
 Cys Ser Glu Cys Gly Lys Ala Phe Asn Asn Arg Ser Asn Phe Asn Lys
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Gly Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val Thr Val Asp Phe	
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Ser Arg Glu Glu Trp Gln Gln Leu Asp Pro Ala Gln Arg Cys Leu Tyr	
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Arg Asp Val Met Leu Glu Leu Tyr Ser His Leu Phe Ala Val Gly Tyr	
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His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu Lys Glu Lys Glu	
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Pro Arg Val Glu Glu Ala Glu Val Ser His Gln Arg Cys Gln Glu Arg	
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Ser Ile Leu Glu Glu Leu Arg Leu Asp Ala Asp Arg Thr Lys Lys Asp	
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Lys Thr Leu Asn Thr Glu Ser Asn Cys Glu Tyr Lys Asp Pro Gly Lys	
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Met Ile Arg Thr Arg Pro His Leu Ala Ser Ser Gln Lys Gln Pro Gln	
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Gly Gln Asn Glu Ser Asn Asp Thr Glu Gln Leu Asp Asp Val Val Gly	
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Ser Gly Gln Leu Phe Ser His Ser Ser Ser Asp Ala Cys Ser Lys Asn	
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Ile His Thr Gly Glu Thr Phe Cys Lys Gly Asn Gln Cys Arg Lys Val	
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cac ctc ttt gcc caa cag aga att cat agt gta gga aac ctc cat gaa	1269
His Leu Phe Ala Gln Gln Arg Ile His Ser Val Gly Asn Leu His Glu	
295 300 305	
tgt ggc aaa tgt gga aaa gcc ttc atg cca caa cta aaa ctc agt gta	1317
Cys Gly Lys Cys Gly Lys Ala Phe Met Pro Gln Leu Lys Leu Ser Val	
310 315 320	

tat ctg aca gat cat aca ggt gat ata ccc tgt ata tgc aag gaa tgt	1365
Tyr Leu Thr Asp His Thr Gly Asp Ile Pro Cys Ile Cys Lys Glu Cys	
325 330 335 340	
ggg aag gtc ttt att cag aga tca gaa ttg ctt acg cac cag aaa aca	1413
Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr His Gln Lys Thr	
345 350 355	
cac act aga aag aag ccc tat aaa tgc cat gac tgt gga aaa gcc ttt	1461
His Thr Arg Lys Lys Pro Tyr Lys Cys His Asp Cys Gly Lys Ala Phe	
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ttc cag atg tta tct ctc ttc aga cat cag aga act cac agt aga gaa	1509
Phe Gln Met Leu Ser Leu Phe Arg His Gln Arg Thr His Ser Arg Glu	
375 380 385	
aaa ctc tat gaa tgc agt gaa tgt ggc aaa ggc ttc tcc caa aac tca	1557
Lys Leu Tyr Glu Cys Ser Glu Cys Gly Lys Gly Phe Ser Gln Asn Ser	
390 395 400	
acc ctc att ata cat cag aaa att cat act ggt gag aga cag tat gca	1605
Thr Leu Ile Ile His Gln Lys Ile His Thr Gly Glu Arg Gln Tyr Ala	
405 410 415 420	
tgc agt gaa tgt ggg aaa gcc ttt acc cag aag tca aca ctc agc ttg	1653
Cys Ser Glu Cys Gly Lys Ala Phe Thr Gln Lys Ser Thr Leu Ser Leu	
425 430 435	
cac cag aga atc cac tca ggg cag aag tcc tat gtg tgt atc gaa tgc	1701
His Gln Arg Ile His Ser Gly Gln Lys Ser Tyr Val Cys Ile Glu Cys	
440 445 450	
ggg cag gcc ttc atc cag aag gca cac ctg att gtc cat caa aga agc	1749
Gly Gln Ala Phe Ile Gln Lys Ala His Leu Ile Val His Gln Arg Ser	
455 460 465	
cac aca gga gaa aaa cct tat cag tgc cac aac tgt ggg aaa tcc ttc	1797
His Thr Gly Glu Lys Pro Tyr Gln Cys His Asn Cys Gly Lys Ser Phe	
470 475 480	
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Ile Ser Lys Ser Gln Leu Asp Ile His His Arg Ile His Thr Gly Glu	
485 490 495 500	
aaa cct tat gaa tgc agt gac tgt gga aaa acc ttc acc caa aag tca	1893
Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Thr Phe Thr Gln Lys Ser	
505 510 515	
cac ctg aat ata cac cag aaa att cat act gga gaa aga cac cat gta	1941
His Leu Asn Ile His Gln Lys Ile His Thr Gly Glu Arg His His Val	
520 525 530	
tgc agt gaa tgc ggg aaa gcc ttc aac cag aag tca ata ctc agc atg	1989
Cys Ser Glu Cys Gly Lys Ala Phe Asn Gln Lys Ser Ile Leu Ser Met	
535 540 545	

cat cag aga att cac acc gga gag aag cct tac aaa tgc agt gaa tgt	2037
His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Glu Cys	
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Gly Lys Ala Phe Thr Ser Lys Ser Gln Phe Lys Glu His Gln Arg Ile	
565 570 575 580	
cac acg ggt gag aaa ccc tat gtg tgc act gaa tgt ggg aag gcc ttc	2133
His Thr Gly Glu Lys Pro Tyr Val Cys Thr Glu Cys Gly Lys Ala Phe	
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aac ggc agg tca aat ttc cat aaa cat caa ata act cac act aga gag	2181
Asn Gly Arg Ser Asn Phe His Lys His Gln Ile Thr His Thr Arg Glu	
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agg cct ttt gtc tgt tac aaa tgt ggg aag gct ttt gtc cag aaa tca	2229
Arg Pro Phe Val Cys Tyr Lys Cys Gly Lys Ala Phe Val Gln Lys Ser	
615 620 625	
gag ttg att acc cat caa aga act cac atg gga gag aaa ccc tat gaa	2277
Glu Leu Ile Thr His Gln Arg Thr His Met Gly Glu Lys Pro Tyr Glu	
630 635 640	
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Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro Gln Leu Lys Val	
645 650 655 660	
cat cag cga att cac acg gga gaa aga cct tat gtg tgt tct gaa tgt	2373
His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val Cys Ser Glu Cys	
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Gly Lys Ala Phe Asn Asn Arg Ser Asn Phe Asn Lys His Gln Thr Thr	
680 685 690	
cat acc aga gac aaa tct tac aaa tgc agt tat tct gtg aaa ggc ttt	2469
His Thr Arg Asp Lys Ser Tyr Lys Cys Ser Tyr Ser Val Lys Gly Phe	
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Thr Lys Gln	
710	
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<213> Homo sapiens

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 20 25 30

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 35 40 45

Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys Gln Leu
 50 55 60

Thr Glu Glu Lys Phe Ile Val Lys Ala Thr Asn Gly Pro Arg Tyr Val
 65 70 75 80

Val Gly Cys Arg Arg Gln Leu Asp Lys Ser Lys Leu Lys Pro Gly Thr
 85 90 95

Arg Val Ala Leu Asp Met Thr Thr Leu Thr Ile Met Arg Tyr Leu Pro
 100 105 110

Arg Glu Val Asp Pro Leu Val Tyr Asn Met Ser His Glu Asp Pro Gly
 115 120 125

Asn Val Ser Tyr Ser Glu Ile Gly Gly Leu Ser Glu Gln Ile Arg Glu
 130 135 140
 Leu Arg Glu Val Ile Glu Leu Pro Leu Thr Asn Pro Glu Leu Phe Gln
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 Arg Val Gly Ile Ile Pro Pro Lys Gly Cys Leu Leu Tyr Gly Pro Pro
 165 170 175
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala Ser Gln Leu Asp
 180 185 190
 Cys Asn Phe Leu Lys Val Val Ser Ser Ser Ile Val Asp Lys Tyr Ile
 195 200 205
 Gly Glu Ser Ala Arg Leu Ile Arg Glu Met Phe Asn Tyr Ala Arg Asp
 210 215 220
 His Gln Pro Cys Ile Ile Phe Met Asp Glu Ile Asp Ala Ile Gly Gly
 225 230 235 240
 Arg Arg Phe Ser Glu Gly Thr Ser Ala Asp Arg Glu Ile Gln Arg Thr
 245 250 255
 Leu Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp Thr Leu His Arg
 260 265 270
 Val Lys Met Thr Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala
 275 280 285
 Leu Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile His Ile Asp Leu Pro
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 Asn Glu Gln Ala Arg Leu Asp Ile Leu Lys Ile His Ala Gly Pro Ile
 305 310 315 320
 Thr Lys His Gly Glu Ile Asp Tyr Glu Ala Ile Val Lys Leu Ser Asp
 325 330 335
 Gly Phe Asn Gly Ala Asp Leu Arg Asn Val Cys Thr Glu Ala Gly Met
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 Phe Ala Ile Arg Ala Asp His Asp Phe Val Val Gln Glu Asp Phe Met
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<210> 14

<211> 1167

<212> DNA

<213> Homo sapiens

<400> 14

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gaaaagtctg aaaatgatct gaaggcccta cagagtgttg ggcagatcgt ggggtgaagtg 180
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Arg Lys Lys Leu Leu Glu His Lys Glu Ile Asp Gly Arg Leu Lys Glu	
15 20 25	
tta agg gaa caa tta aaa gaa ctt acc aag cag tat gaa aag tct gaa	148
Leu Arg Glu Gln Leu Lys Glu Leu Thr Lys Gln Tyr Glu Lys Ser Glu	
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aat gat ctg aag gcc cta cag agt gtt ggg cag atc gtg ggt gaa gtg	196
Asn Asp Leu Lys Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val	
45 50 55 60	
ctt aaa cag tta act gaa gaa aaa ttc att gtt aaa gct acc aat gga	244
Leu Lys Gln Leu Thr Glu Glu Lys Phe Ile Val Lys Ala Thr Asn Gly	
65 70 75	
cca aga tat gtt gtg ggt tgt cgt cga cag ctt gac aaa agt aag ctg	292
Pro Arg Tyr Val Val Gly Cys Arg Arg Gln Leu Asp Lys Ser Lys Leu	
80 85 90	
aag cca gga aca aga gtt gct ttg gat atg act aca cta act atc atg	340
Lys Pro Gly Thr Arg Val Ala Leu Asp Met Thr Thr Leu Thr Ile Met	
95 100 105	
aga tat ttg ccg aga gag gtg gat cca ctg gtt tat aac atg tct cat	388
Arg Tyr Leu Pro Arg Glu Val Asp Pro Leu Val Tyr Asn Met Ser His	
110 115 120	
gag gac cct ggg aat gtt tct tat tct gag att gga ggg cta tca gaa	436
Glu Asp Pro Gly Asn Val Ser Tyr Ser Glu Ile Gly Gly Leu Ser Glu	
125 130 135 140	
cag atc cgg gaa tta aga gag gtg ata gaa tta cct ctt aca aac cca	484
Gln Ile Arg Glu Leu Arg Glu Val Ile Glu Leu Pro Leu Thr Asn Pro	
145 150 155	
gag tta ttt cag cgt gta gga ata ata cct cca aaa ggc tgt ttg tta	532
Glu Leu Phe Gln Arg Val Gly Ile Ile Pro Pro Lys Gly Cys Leu Leu	
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tat gga cca cca ggt acg gga aaa aca ctc ttg gca cga gcc gtt gct	580
Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala	
175 180 185	
agc cag ctg gac tgc aat ttc tta aag gtt gta tct agt tct att gta	628
Ser Gln Leu Asp Cys Asn Phe Leu Lys Val Val Ser Ser Ser Ile Val	
190 195 200	
gac aag tac att ggt gaa agt gct cgt ttg atc aga gaa atg ttt aat	676
Asp Lys Tyr Ile Gly Glu Ser Ala Arg Leu Ile Arg Glu Met Phe Asn	
205 210 215 220	
tat gct aga gat cat caa cca tgc atc att ttt atg gat gaa ata gat	724
Tyr Ala Arg Asp His Gln Pro Cys Ile Ile Phe Met Asp Glu Ile Asp	
225 230 235	

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gct att ggt ggt cgt cgg ttt tct gag ggt act tca gct gac aga gag 772
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      240                      245                      250

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Ile Gln Arg Thr Leu Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp
      255                      260                      265

act ctg cat aga gtt aaa atg acc atg gct aca aac aga cca gat aca 868
Thr Leu His Arg Val Lys Met Thr Met Ala Thr Asn Arg Pro Asp Thr
      270                      275                      280

ctg gat cct gct ttg ctg cgt cca gga aga tta gat aga aaa ata cat 916
Leu Asp Pro Ala Leu Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile His
285                      290                      295                      300

att gat ttg cca aat gaa caa gca aga tta gac ata ctg aaa atc cat 964
Ile Asp Leu Pro Asn Glu Gln Ala Arg Leu Asp Ile Leu Lys Ile His
      305                      310                      315

gca ggt ccc att aca aag cat ggt gaa ata gat tat gaa gca att gtg 1012
Ala Gly Pro Ile Thr Lys His Gly Glu Ile Asp Tyr Glu Ala Ile Val
      320                      325                      330

aag ctt tcg gat ggc ttt aat gga gca gat ctg aga aat gtt tgt act 1060
Lys Leu Ser Asp Gly Phe Asn Gly Ala Asp Leu Arg Asn Val Cys Thr
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gaa gca ggt atg ttc gca att cgt gct gat cat gat ttt gta gta cag 1108
Glu Ala Gly Met Phe Ala Ile Arg Ala Asp His Asp Phe Val Val Gln
      350                      355                      360

gaa gac ttc atg aaa gca gtc aga aaa gtg gct gat tct aag aag ctg 1156
Glu Asp Phe Met Lys Ala Val Arg Lys Val Ala Asp Ser Lys Lys Leu
365                      370                      375                      380

gag tct aaa ttg gac tac aaa cct gtg taatttactg taagattttt 1203
Glu Ser Lys Leu Asp Tyr Lys Pro Val
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cagcaagtta caaagggaaa gtgttgaagc ttttcatatt tgctgcgtga gcatttttgta 1443

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<212> PRT

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<213> Homo sapiens

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Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln Lys
 35 40 45

Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro Arg
 50 55 60

Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile Ile
 65 70 75 80

Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu Ala
 85 90 95

Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp Met
 100 105 110

Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser Glu
 115 120 125

Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser Pro
 130 135 140

Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile Val
 145 150 155 160

Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn Ile
 165 170 175

Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr Val
 180 185 190

Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg Trp
 195 200 205

Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg
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<210> 17

<211> 669

<212> DNA

<213> Homo sapiens

<400> 17

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gggtaccccc ggtcagacgt ggacctgtac caagtccgca ccgccaggca caacatcata 240
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 Met Ser Asp Glu Glu Ala Arg Gln Ser Gly Gly Ser Ser Gln Ala
 1 5 10 15
 ggc gtc gtg act gtc agc gac gtc cag gag ctg atg cgg cgc aag gag 217
 Gly Val Val Thr Val Ser Asp Val Gln Glu Leu Met Arg Arg Lys Glu
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 Glu Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln
 35 40 45
 aaa ggc att ggg atg aac gag ccg ctg gtg gac tgt gag ggc tac ccc 313
 Lys Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro
 50 55 60
 cgg tca gac gtg gac ctg tac caa gtc cgc acc gcc agg cac aac atc 361
 Arg Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile
 65 70 75
 ata tgc ctg cag aat gat cac aag gca gtg atg aag cag gtg gag gag 409
 Ile Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu
 80 85 90 95

gcc ctg cac cag ctg cac gct cgc gac aag gag aag cag gcc cgg gac 457
 Ala Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp
 100 105 110

atg gct gag gcc cac aaa gag gcc atg agc cgc aaa ctg ggt cag agt 505
 Met Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser
 115 120 125

gag agc cag ggc cct cca cgg gcc ttc gcc aaa gtg aac agc atc agc 553
 Glu Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser
 130 135 140

ccc ggc tcc cca gcc agc atc gcg ggt ctg caa gtg gat gat gag att 601
 Pro Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile
 145 150 155

gtg gag ttc ggc tct gtg aac acc cag aac ttc cag tca ctg cat aac 649
 Val Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn
 160 165 170 175

att ggc agt gtg gtg cag cac agt gag ggg aag ccc ctg aat gtg aca 697
 Ile Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr
 180 185 190

gtg atc cgc agg ggg gaa aaa cac cag ctt aga ctt gtt cca aca cgc 745
 Val Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg
 195 200 205

tgg gca gga aaa gga ctg ctg ggc tgc aac att att cct ctg caa aga 793
 Trp Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg
 210 215 220

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 <211> 506
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 35 40 45
 Ser Ser Thr Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser
 50 55 60
 Ser Gly Ser Thr Ser Ser Arg Ser Arg Leu Tyr Arg Lys Lys Arg Val
 65 70 75 80
 Pro Glu Pro Ser Arg Arg Ala Arg Arg Ala Pro Leu Gly Thr Asn Phe
 85 90 95
 Val Asp Arg Leu Pro Gln Ala Val Arg Asn Arg Val Gln Ala Leu Arg
 100 105 110
 Asn Ile Gln Asp Glu Cys Asp Lys Val Asp Thr Leu Phe Leu Lys Ala
 115 120 125
 Ile His Asp Leu Glu Arg Lys Tyr Ala Glu Leu Asn Lys Pro Leu Tyr
 130 135 140
 Asp Arg Arg Phe Gln Ile Ile Asn Ala Glu Tyr Glu Pro Thr Glu Glu
 145 150 155 160
 Glu Cys Glu Trp Asn Ser Glu Asp Glu Glu Phe Ser Ser Asp Glu Glu
 165 170 175
 Val Gln Asp Asn Thr Pro Ser Glu Met Pro Pro Leu Glu Gly Glu Glu
 180 185 190
 Glu Glu Asn Pro Lys Glu Asn Pro Glu Val Lys Ala Glu Glu Lys Glu
 195 200 205
 Val Pro Lys Glu Ile Pro Glu Val Lys Asp Glu Glu Lys Glu Val Ala
 210 215 220
 Lys Glu Ile Pro Glu Val Lys Ala Glu Glu Lys Ala Asp Ser Lys Asp
 225 230 235 240
 Cys Met Glu Ala Thr Pro Glu Val Lys Glu Asp Pro Lys Glu Val Pro
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 Gln Val Lys Ala Asp Asp Lys Glu Gln Pro Lys Ala Thr Glu Ala Lys
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 Ala Arg Ala Ala Val Arg Glu Thr His Lys Arg Val Pro Glu Glu Arg
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 Leu Arg Asp Ser Val Asp Leu Lys Arg Ala Arg Lys Gly Lys Pro Lys
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 Arg Glu Asp Pro Lys Gly Ile Pro Asp Tyr Trp Leu Ile Val Leu Lys
 305 310 315 320
 Asn Val Asp Lys Leu Gly Pro Met Ile Gln Lys Tyr Asp Glu Pro Ile
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Leu Lys Phe Leu Ser Asp Val Ser Leu Lys Phe Ser Lys Pro Gly Gln
 340 345 350

Pro Val Ser Tyr Thr Phe Glu Phe His Phe Leu Pro Asn Pro Tyr Phe
 355 360 365

Arg Asn Glu Val Leu Val Lys Thr Tyr Ile Ile Lys Ala Lys Pro Asp
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His Asn Asp Pro Phe Phe Ser Trp Gly Trp Glu Ile Glu Asp Cys Lys
 385 390 395 400

Gly Cys Lys Ile Asp Arg Arg Arg Gly Lys Asp Val Thr Val Thr Thr
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Thr Gln Ser Arg Thr Thr Ala Thr Gly Glu Ile Glu Ile Gln Pro Arg
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Val Val Pro Asn Ala Ser Phe Phe Asn Phe Phe Ser Pro Pro Glu Ile
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Pro Met Ile Gly Lys Leu Glu Pro Arg Glu Asp Ala Ile Leu Asp Glu
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Asp Phe Glu Ile Gly Gln Ile Leu His Asp Asn Val Ile Leu Lys Ser
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Thr Ser Asp Ser Gly Glu Glu Ser Asp Ser Ser Ser Ser Ser Ser Ser	
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Thr Ser Asp Ser Ser Ser Ser Ser Ser Thr Ser Gly Ser Ser Ser Gly	
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Ser Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Ser Arg Ser Arg	
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Leu Tyr Arg Lys Lys Arg Val Pro Glu Pro Ser Arg Arg Ala Arg Arg	
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Ala Pro Leu Gly Thr Asn Phe Val Asp Arg Leu Pro Gln Ala Val Arg	
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aat cgt gtg caa gcg ctt aga aac att caa gat gaa tgt gac aag gta	628
Asn Arg Val Gln Ala Leu Arg Asn Ile Gln Asp Glu Cys Asp Lys Val	
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Asp Thr Leu Phe Leu Lys Ala Ile His Asp Leu Glu Arg Lys Tyr Ala	
125 130 135	
gaa ctc aac aag cct ctg tat gat agg cgg ttt caa atc atc aat gca	724
Glu Leu Asn Lys Pro Leu Tyr Asp Arg Arg Phe Gln Ile Ile Asn Ala	
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Glu Tyr Glu Pro Thr Glu Glu Glu Cys Glu Trp Asn Ser Glu Asp Glu	
155 160 165	
gag ttc agc agt gat gag gag gtg cag gat aac acc cct agt gaa atg	820
Glu Phe Ser Ser Asp Glu Glu Val Gln Asp Asn Thr Pro Ser Glu Met	
170 175 180 185	
cct ccc tta gag ggt gag gaa gaa gaa aac cct aaa gaa aac cca gag	868
Pro Pro Leu Glu Gly Glu Glu Glu Glu Asn Pro Lys Glu Asn Pro Glu	
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gtg aaa gct gaa gag aag gaa gtt cct aaa gaa att cct gag gtg aag	916
Val Lys Ala Glu Glu Lys Glu Val Pro Lys Glu Ile Pro Glu Val Lys	
205 210 215	
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Asp Glu Glu Lys Glu Val Ala Lys Glu Ile Pro Glu Val Lys Ala Glu	
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Lys Arg Val Pro Glu Glu Arg Leu Arg Asp Ser Val Asp Leu Lys Arg	
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Ala Arg Lys Gly Lys Pro Lys Arg Glu Asp Pro Lys Gly Ile Pro Asp	
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Gln Lys Tyr Asp Glu Pro Ile Leu Lys Phe Leu Ser Asp Val Ser Leu	
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Phe Leu Pro Asn Pro Tyr Phe Arg Asn Glu Val Leu Val Lys Thr Tyr	
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Ile Ile Lys Ala Lys Pro Asp His Asn Asp Pro Phe Phe Ser Trp Gly	
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Trp Glu Ile Glu Asp Cys Lys Gly Cys Lys Ile Asp Arg Arg Arg Gly	
395 400 405	
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Lys Asp Val Thr Val Thr Thr Thr Gln Ser Arg Thr Thr Ala Thr Gly	
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ttc ttt agt cct cct gag att cct atg att ggg aag ctg gaa cca cga	1636
Phe Phe Ser Pro Pro Glu Ile Pro Met Ile Gly Lys Leu Glu Pro Arg	
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Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile Gly Pro Pro Asp Thr
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Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu Thr Phe Pro Lys Asp
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 Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile Ser Ile Leu His Glu
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 Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro Glu Glu Arg Trp Leu
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 Pro Ile His Thr Val Glu Thr Ile Met Ile Ser Val Ile Ser Met Leu
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 Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val Asp Ala Ala Lys Glu
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 <211> 510
 <212> DNA
 <213> Homo sapiens

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Arg Gln Leu Ala Glu Leu Asn Lys Asn Pro Val Glu Gly Phe Ser Ala
      15          20          25

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Gly Leu Ile Asp Asp Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile
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ggc cct cca gat aca ctt tat gaa ggt ggt gtt ttt aag gct cat ctt 195
Gly Pro Pro Asp Thr Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu
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Thr Phe Pro Lys Asp Tyr Pro Leu Arg Pro Pro Lys Met Lys Phe Ile
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Thr Glu Ile Trp His Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile
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tct att ctt cat gag cct ggg gaa gat aag tat ggt tat gaa aag cca 339
Ser Ile Leu His Glu Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro
      95          100          105

gag gaa cgc tgg ctc cct atc cac act gtg gaa acc atc atg att agt 387
Glu Glu Arg Trp Leu Pro Ile His Thr Val Glu Thr Ile Met Ile Ser
      110          115          120

gtc att tct atg ctg gca gac cct aat gga gac tca cct gct aat gtt 435
Val Ile Ser Met Leu Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val
      125          130          135

gat gct gcg aaa gaa tgg agg gaa gat aga aat gga gaa ttt aaa aga 483
Asp Ala Ala Lys Glu Trp Arg Glu Asp Arg Asn Gly Glu Phe Lys Arg
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aaa gtt gcc cgc tgt gta aga aaa agc caa gag act gct ttt gag 528
Lys Val Ala Arg Cys Val Arg Lys Ser Gln Glu Thr Ala Phe Glu
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<212> PRT

<213> Homo sapiens

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Ser	Ala	Arg	Glu	His	His	Ile	Pro	Cys	Pro	Glu	His	Tyr	Asn	Gly	Phe
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Cys	Met	His	Gly	Lys	Cys	Glu	His	Ser	Ile	Asn	Met	Gln	Glu	Pro	Ser
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Cys	Arg	Cys	Asp	Ala	Gly	Tyr	Thr	Gly	Gln	His	Cys	Glu	Lys	Lys	Asp
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Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val
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Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val
325 330 335

Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His
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<211> 1122

<212> DNA

<213> Homo sapiens

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1122

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 <213> Homo sapiens

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 Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr Asp Asp Arg
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 80 85 90
 tgc aac aat gac tat gtg cct gtg tgt ggc tcc aat ggg gag agc tac 697
 Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly Glu Ser Tyr
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 cag aat gag tgt tac ctg cga cag gct gca tgc aaa cag cag agt gag 745
 Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln Gln Ser Glu
 115 120 125

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Pro Gln Leu Leu Asn Met Tyr Ile His Met Asp Glu Asp Val Gly Asp
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<212> DNA

<213> Homo sapiens

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 Phe Ser Val Asp Ser Ile Thr Ser Gln Glu Ser Lys Glu Pro Val Phe
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 Phe Ile Leu Ser Ser Ser Pro Arg Asn Leu Gly Phe Glu Thr Ser Ala
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 Arg Phe Leu Glu Ala Arg Ser Leu Ala Val Ala Met Gly Asp Thr Val
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 gtg gag cct gcc ccc ttg aag cca act tct gag ccc act tct ggc cca 213
 Val Glu Pro Ala Pro Leu Lys Pro Thr Ser Glu Pro Thr Ser Gly Pro
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 cca ggg aat aat ggg ggg tcc ctg cta agt gtc atc acg gag ggg gtc 261
 Pro Gly Asn Asn Gly Gly Ser Leu Leu Ser Val Ile Thr Glu Gly Val
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gat gag atg ggg gcc gct gtg gcc tca ggc aca gcc aaa gga gca aga Asp Glu Met Gly Ala Ala Val Ala Ser Gly Thr Ala Lys Gly Ala Arg 115 120 125	501
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Asp Thr Gly Leu Ser Pro Ser Lys Arg Thr His Gln Arg Ser Lys Ser	
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Asp Ala Thr Ala Ser Ile Ser Leu Ser Ser Asn Leu Lys Arg Thr Ala	
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Arg Glu Phe Ile Lys Ser Leu Met Ala Ile Gly Lys Arg Leu Ala Thr	
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Leu Pro Thr Lys Glu Gln Lys Thr Gln Arg Leu Ile Ser Glu Leu Ser	
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Asn Ser Lys Asp Lys Ala Pro Tyr Leu Ile Tyr Val Glu Val Leu Glu	
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Cys Glu Asn Phe Asp Thr Thr Ser Val Pro Ala Arg Ile Pro Glu Asn	
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Ala	Ala	Gly	Asp	Ile	Arg	Arg	Arg	Leu	Ser	Glu	Gln	Leu	Ala	His	Thr	
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ccg	aca	gcc	ttc	aaa	cga	gac	cca	gaa	gat	cct	tct	gca	gtt	gct	ctc	1749
Pro	Thr	Ala	Phe	Lys	Arg	Asp	Pro	Glu	Asp	Pro	Ser	Ala	Val	Ala	Leu	
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Lys	Glu	Pro	Trp	Gln	Glu	Lys	Val	Arg	Arg	Ile	Arg	Glu	Gly	Ser	Pro	
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tac	ggc	cat	ctc	ccc	aat	tgg	cgg	ctc	ctg	tca	gtc	att	gtc	aag	tgt	1845
Tyr	Gly	His	Leu	Pro	Asn	Trp	Arg	Leu	Leu	Ser	Val	Ile	Val	Lys	Cys	
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Gly	Asp	Asp	Leu	Arg	Gln	Glu	Leu	Leu	Ala	Phe	Gln	Val	Leu	Lys	Gln	
	580						585					590				
ctg	cag	tcc	att	tgg	gaa	cag	gag	cga	gtg	ccc	ctt	tgg	atc	aag	cca	1941
Leu	Gln	Ser	Ile	Trp	Glu	Gln	Glu	Arg	Val	Pro	Leu	Trp	Ile	Lys	Pro	
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Ile	Gln	Asp	Ser	Cys	Glu	Ile	Thr	Thr	Asp	Ser	Gly	Met	Ile	Glu	Pro	
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gtg	gtc	aat	gct	gtg	tcc	atc	cat	cag	gtg	aag	aaa	cag	tca	cag	ctc	2037
Val	Val	Asn	Ala	Val	Ser	Ile	His	Gln	Val	Lys	Lys	Gln	Ser	Gln	Leu	
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tcc	ttg	ctc	gat	tac	ttc	cta	cag	gag	cac	ggc	agt	tac	acc	act	gag	2085
Ser	Leu	Leu	Asp	Tyr	Phe	Leu	Gln	Glu	His	Gly	Ser	Tyr	Thr	Thr	Glu	
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gca	ttc	ctc	agt	gca	cag	cgc	aat	ttt	gtg	caa	agt	tgt	gct	ggg	tac	2133
Ala	Phe	Leu	Ser	Ala	Gln	Arg	Asn	Phe	Val	Gln	Ser	Cys	Ala	Gly	Tyr	
	660						665					670				
tgc	ttg	gtc	tgc	tac	ctg	ctg	caa	gtc	aag	gac	aga	cac	aat	ggg	aat	2181
Cys	Leu	Val	Cys	Tyr	Leu	Leu	Gln	Val	Lys	Asp	Arg	His	Asn	Gly	Asn	
	675					680					685					
atc	ctt	ttg	gac	gca	gaa	ggc	cac	atc	atc	cac	atc	gac	ttt	ggc	ttc	2229
Ile	Leu	Leu	Asp	Ala	Glu	Gly	His	Ile	Ile	His	Ile	Asp	Phe	Gly	Phe	
690					695					700					705	
atc	ctc	tcc	agc	tca	ccc	cga	aat	ctg	ggc	ttt	gag	acg	tca	gcc	ttt	2277
Ile	Leu	Ser	Ser	Ser	Pro	Arg	Asn	Leu	Gly	Phe	Glu	Thr	Ser	Ala	Phe	
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Lys Leu Thr Thr Glu Phe Val Asp Val Met Gly Gly Leu Asp Gly Asp
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atg ttc aac tac tat aag atg ctg atg ctg caa ggg ctg att gcc gct 2373
Met Phe Asn Tyr Tyr Lys Met Leu Met Leu Gln Gly Leu Ile Ala Ala
740 745 750

cgg aaa cac atg gac aag gtg gtg cag atc gtg gag atc atg cag caa 2421
Arg Lys His Met Asp Lys Val Val Gln Ile Val Glu Ile Met Gln Gln
755 760 765

ggg tct cag ctt cct tgc ttc cat ggc tcc agc acc att cga aac ctc 2469
Gly Ser Gln Leu Pro Cys Phe His Gly Ser Ser Thr Ile Arg Asn Leu
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790 795 800

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805 810 815

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820 825

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 Ile Ile Phe Met Pro Asn Gly Tyr Ile Thr Gln Cys Pro Asn Leu Asn
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 Cys Gly Glu Asn Ser Glu Cys Lys Asn Trp Asn Thr Lys Ala Thr Cys
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 Gly Tyr Ile Arg Val Asp Asp Phe Ser Cys Thr Glu His Asp Glu Cys
 465 470 475 480
 Gly Ser Gly Gln His Asn Cys Asp Glu Asn Ala Ile Cys Thr Asn Thr
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 Ser Cys Ile Asp Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp
 595 600 605

Asn Asp Ser Ala Cys Ile Asn Leu Ala Gly Gly Phe Asp Cys Leu Cys
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 Pro Ser Gly Pro Ser Cys Ser Gly Asp Cys Pro His Glu Gly Gly Leu
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 645 650 655
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 Arg Val Thr Ser Gln Cys Leu Asp Gln Asn Gly His Lys Leu Tyr Arg
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 Ser Gly Asp Asn Trp Thr His Ser Cys Gln Gln Cys Arg Cys Leu Glu
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 Gly Glu Val Asp Cys Trp Pro Leu Thr Cys Pro Asn Leu Ser Cys Glu
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 Tyr Thr Ala Ile Leu Glu Gly Glu Cys Cys Pro Arg Cys Val Ser Asp
 740 745 750
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Asp Leu Val Asn Thr Thr Leu Gly Val Ala Gln Val Ser Gly Met His
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Asn Ala Ser Lys Ala Phe Leu Phe Gln Asp Ile Glu Arg Glu Ile His
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Gly Val Ile Leu Ser Ile Arg Glu Leu Glu His Ser Tyr Phe Glu Leu
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Trp His Lys Val Ala Leu Ser Val Ser Ala Ser His Leu Leu Leu His	
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His Gly Leu Phe Lys Gly Ile Ile Gln Asp Gly Lys Ile Ile Phe Met	
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Asp Gly Lys Ile Phe Cys Arg Arg Thr Ala Cys Asp Cys Gln Asn Pro	
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Ser Ala Asp Leu Phe Cys Cys Pro Glu Cys Asp Thr Arg Val Thr Ser	
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Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
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Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
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His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
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Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Val Arg Leu His
 115 120 125

Tyr Arg Ser Gly Ser His Arg Pro His Thr Glu Val Phe Pro Tyr Ile
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His Leu Ile Leu His Ile Asp Cys Asn Lys Ile Tyr Glu Arg Val Val
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 Glu Lys Pro Ser Thr Asp Leu Pro Leu Gly Thr Thr Phe Trp Leu Gly
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<212> DNA

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Gly Val Asp Pro Ser Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu	
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Gly Glu Ser Thr Thr Gly Val Arg Gln Val Pro Gly Leu His Asn Gly	
40 45 50	
acg aaa gcc ttt ctc ttt caa gat act ccc aga agc ata aaa gca tcc	306
Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser	
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Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu	
75 80 85	
ttt act att ttg gtg acc cta aaa cag acc cac tta aat tca gga gtt	402
Phe Thr Ile Leu Val Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val	
90 95 100	
att ctc tca att cac cac ttg gat cac agg tac ctg gaa ctg gaa agt	450
Ile Leu Ser Ile His His Leu Asp His Arg Tyr Leu Glu Leu Glu Ser	
105 110 115	
agt ggc cat cgg aat gaa gtc aga ctg cat tac cgc tca ggc agt cac	498
Ser Gly His Arg Asn Glu Val Arg Leu His Tyr Arg Ser Gly Ser His	
120 125 130	
cgc cct cac aca gaa gtg ttt cct tac att ttg gct gat gac aag tgg	546
Arg Pro His Thr Glu Val Phe Pro Tyr Ile Leu Ala Asp Asp Lys Trp	
135 140 145 150	
cac aag ctc tcc tta gcc atc agt gct tcc cat ttg att tta cac att	594
His Lys Leu Ser Leu Ala Ile Ser Ala Ser His Leu Ile Leu His Ile	
155 160 165	
gac tgc aat aaa att tat gaa agg gta gta gaa aag ccc tcc aca gac	642
Asp Cys Asn Lys Ile Tyr Glu Arg Val Val Glu Lys Pro Ser Thr Asp	
170 175 180	
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Leu Pro Leu Gly Thr Thr Phe Trp Leu Gly Gln Arg Asn Asn Ala His	
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Gly Tyr Phe Lys Gly Ile Met Gln Asp Val Gln Leu Leu Val Met Pro	
200 205 210	
cag gga ttt att gct cag tgc cca gat ctt aat cgc acc tgt cca act	786
Gln Gly Phe Ile Ala Gln Cys Pro Asp Leu Asn Arg Thr Cys Pro Thr	
215 220 225 230	

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Cys Asn Asp Phe His Gly Leu Val Gln Lys Ile Met Glu Leu Gln Asp	
235 240 245	
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Ile Leu Ala Lys Thr Ser Ala Lys Leu Ser Arg Ala Glu Gln Arg Met	
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Asn Arg Leu Asp Gln Cys Tyr Cys Glu Arg Thr Cys Thr Met Lys Gly	
265 270 275	
acc acc tac cga gaa ttt gag tcc tgg ata gac ggc tgt aag aac tgc	978
Thr Thr Tyr Arg Glu Phe Glu Ser Trp Ile Asp Gly Cys Lys Asn Cys	
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Pro Asp Cys Pro Leu Lys Ser Ala Leu Ala Tyr Val Asp Gly Lys Cys	
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Cys Lys Glu Cys Lys Ser Ile Cys Gln Phe Gln Gly Arg Thr Tyr Phe	
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Glu Gly Glu Arg Asn Thr Val Tyr Ser Ser Ser Gly Val Cys Val Leu	
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Tyr Glu Cys Lys Asp Gln Thr Met Lys Leu Val Glu Ser Ser Gly Cys	
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Pro Ala Leu Asp Cys Pro Glu Ser His Gln Ile Thr Leu Ser His Ser	
375 380 385 390	
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Cys Cys Lys Val Cys Lys Gly Tyr Asp Phe Cys Ser Glu Arg His Asn	
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Cys Met Glu Asn Ser Ile Cys Arg Asn Leu Asn Asp Arg Ala Val Cys	
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Ser Cys Arg Asp Gly Phe Arg Ala Leu Arg Glu Asp Asn Ala Tyr Cys	
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Glu Asp Ile Asp Glu Cys Ala Glu Gly Arg His Tyr Cys Arg Glu Asn	
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Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys Thr Glu His Asp Glu Cys	
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Ile Thr Asn Gln His Asn Cys Asp Glu Asn Ala Leu Cys Phe Asn Thr	
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Val Gly Gly His Asn Cys Val Cys Lys Pro Gly Tyr Thr Gly Asn Gly	
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acg aca tgc aaa gca ttt tgc aaa gat ggc tgt agg aat gga gga gcc	1698
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Cys Ile Ala Ala Asn Val Cys Ala Cys Pro Gln Gly Phe Thr Gly Pro	
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Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser Asp Gly Phe Val Gln Cys	
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Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro Gly Trp Tyr His Cys Glu	
570 575 580	
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Cys Arg Asp Gly Tyr His Asp Asn Gly Met Phe Ser Pro Ser Gly Glu	
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Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr Gly Arg His Ser Cys Ala	
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Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly Gly Tyr Asp Cys Arg Cys	
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Pro His Gly Lys Asn Cys Thr Gly Asp Cys Ile His Asp Gly Lys Val	
635 640 645	
aag cac aat ggt cag att tgg gtg ttg gaa aat gac agg tgc tct gtg	2082
Lys His Asn Gly Gln Ile Trp Val Leu Glu Asn Asp Arg Cys Ser Val	
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Cys Ser Cys Gln Asn Gly Phe Val Met Cys Arg Arg Met Val Cys Asp	
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Cys Glu Asn Pro Thr Val Asp Leu Phe Cys Cys Pro Glu Cys Asp Pro	
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Arg Leu Ser Ser Gln Cys Leu His Gln Asn Gly Glu Thr Leu Tyr Asn	
695 700 705 710	
agt ggt gac acc tgg gtc cag aat tgt caa cag tgc cgc tgc ttg caa	2274
Ser Gly Asp Thr Trp Val Gln Asn Cys Gln Gln Cys Arg Cys Leu Gln	
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Gly Glu Val Asp Cys Trp Pro Leu Pro Cys Pro Asp Val Glu Cys Glu	
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Phe Ser Ile Leu Pro Glu Asn Glu Cys Cys Pro Arg Cys Val Thr Asp	
745 750 755	
cct tgc cag gct gac acc atc cgc aat gac atc acc aag act tgc ctg	2418
Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp Ile Thr Lys Thr Cys Leu	
760 765 770	
gac gaa atg aat gtg gtt cgc ttc acc ggg tcc tct tgg atc aaa cat	2466
Asp Glu Met Asn Val Val Arg Phe Thr Gly Ser Ser Trp Ile Lys His	
775 780 785 790	
ggc act gag tgt act ctc tgc cag tgc aag aat ggc cac atc tgt tgc	2514
Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys Asn Gly His Ile Cys Cys	
795 800 805	
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Ser Val Asp Pro Gln Cys Leu Gln Glu Leu	
810 815	
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 <213> Homo sapiens

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 35 40 45
 Glu Met Met Glu Glu Lys Glu Glu Ile Arg Lys Ser Lys Ser Val Ile
 50 55 60
 Val Pro Ser Gly Ala Pro Lys Lys Glu His Val Asn Val Val Phe Ile
 65 70 75 80
 Gly His Val Asp Ala Gly Lys Ser Thr Ile Gly Gly Gln Ile Met Phe
 85 90 95
 Leu Thr Gly Met Ala Asp Lys Arg Thr Leu Glu Lys Tyr Glu Arg Glu
 100 105 110
 Ala Glu Glu Lys Asn Arg Glu Thr Trp Tyr Leu Ser Trp Ala Leu Asp
 115 120 125
 Thr Asn Gln Glu Glu Arg Asp Lys Gly Lys Thr Val Glu Val Gly Arg
 130 135 140
 Ala Tyr Phe Glu Thr Glu Arg Lys His Phe Thr Ile Leu Asp Ala Pro
 145 150 155 160
 Gly His Lys Ser Phe Val Pro Asn Met Ile Gly Gly Ala Ser Glu Ala
 165 170 175
 Asp Leu Ala Val Leu Val Ile Ser Ala Arg Lys Gly Glu Phe Glu Thr
 180 185 190
 Gly Phe Glu Lys Gly Gly Gln Thr Arg Glu His Ala Met Phe Gly Lys
 195 200 205
 Thr Ala Gly Val Lys His Leu Ile Val Leu Ile Asn Lys Met Asp Asp
 210 215 220
 Pro Thr Val Asn Trp Gly Ile Glu Arg Tyr Glu Glu Cys Lys Glu Lys
 225 230 235 240
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gggccccccag aagaaagtgg ccaggaaatg atggaggaaa aagaggaaat aagaaaatcc 180
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gaagtgggtc gtgcctatct tgaacagaa aggaaacatt tcacaatttt agatgccctt 480
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aaggttccaa ttcagccggt acc atg gaa ctt tca gaa cct gtt gta gaa aat 173
Met Glu Leu Ser Glu Pro Val Val Glu Asn
1 5 10

gga gag gtg gaa atg gcc cta gaa gaa tca tgg gag cac agt aaa gaa 221
Gly Glu Val Glu Met Ala Leu Glu Glu Ser Trp Glu His Ser Lys Glu
15 20 25

gta agt gaa gcc gag cct ggg ggt ggt tcc tcg gga gat tca ggg ccc 269
Val Ser Glu Ala Glu Pro Gly Gly Gly Ser Ser Gly Asp Ser Gly Pro
30 35 40

cca gaa gaa agt ggc cag gaa atg atg gag gaa aaa gag gaa ata aga 317
Pro Glu Glu Ser Gly Gln Glu Met Met Glu Glu Lys Glu Glu Ile Arg
45 50 55

aaa tcc aaa tct gtg atc gta ccc tca ggt gca cct aag aaa gaa cac 365
Lys Ser Lys Ser Val Ile Val Pro Ser Gly Ala Pro Lys Lys Glu His
60 65 70

gta aat gta gta ttc att ggc cat gta gac gct ggc aag tca acc atc 413
Val Asn Val Val Phe Ile Gly His Val Asp Ala Gly Lys Ser Thr Ile
75 80 85 90

gga gga cag ata atg ttt ttg act gga atg gct gac aaa aga aca ctg 461
Gly Gly Gln Ile Met Phe Leu Thr Gly Met Ala Asp Lys Arg Thr Leu
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Glu Lys Tyr Glu Arg Glu Ala Glu Glu Lys Asn Arg Glu Thr Trp Tyr
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Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp Lys Gly Lys
125 130 135

aca gtc gaa gtg ggt cgt gcc tat ttt gaa aca gaa agg aaa cat ttc 605
Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Arg Lys His Phe
140 145 150

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Thr Ile Leu Asp Ala Pro Gly His Lys Ser Phe Val Pro Asn Met Ile
155 160 165 170

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175 180 185

aaa gga gag ttt gaa act gga ttt gaa aaa ggt gga cag aca aga gaa 749
Lys Gly Glu Phe Glu Thr Gly Phe Glu Lys Gly Gly Gln Thr Arg Glu
190 195 200

cat gcg atg ttt ggc aaa acg gca gga gta aaa cat tta ata gtg ctt 797
His Ala Met Phe Gly Lys Thr Ala Gly Val Lys His Leu Ile Val Leu
205 210 215

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Ile Asn Lys Met Asp Asp Pro Thr Val Asn Trp Gly Ile Glu Arg Tyr	
220 225 230	
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Ser Pro Lys Lys Asp Ile His Phe Met Pro Cys Ser Gly Leu Thr Gly	
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Ala Asn Ile Lys Glu Gln Ser Asp Phe Cys Pro Trp Tyr Thr Gly Leu	
270 275 280	
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Gln Leu Val Met Met Pro Asn Lys His Asn Val Glu Val Leu Gly Ile	
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Leu Ser Asp Asp Thr Glu Thr Asp Phe Val Ala Pro Gly Glu Asn Leu	
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Lys Ile Arg Leu Lys Gly Ile Glu Glu Glu Glu Ile Leu Pro Glu Phe	
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380 385 390	
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Val Gln Ile Val Ile Ile Glu His Lys Ser Ile Ile Cys Pro Gly Tyr	
395 400 405 410	
 aat gcg gtg ctg cac att cat act tgt att gag gaa gtt gag ata aca	1421
Asn Ala Val Leu His Ile His Thr Cys Ile Glu Glu Val Glu Ile Thr	
415 420 425	
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 460 465 470

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 Gly Arg Phe Thr Leu Arg Asp Glu Gly Lys Thr Ile Ala Ile Gly Lys
 475 480 485 490

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 Val Leu Lys Leu Val Pro Glu Lys Asp
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<211> 24

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer P1

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<210> 44

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P2

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34

<210> 45

<211> 21

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: consensus
sequence

<220>

<223> all "Xaa" amino acids are unidentified

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His	Gln	Arg	Xaa	His
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<211> 7

<212> PRT

<213> Bovine sp.

<400> 46

Val	Leu	Asn	Ile	Ser	Leu	Trp
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<210> 47

<211> 17

<212> PRT

<213> Bovine sp.

<400> 47

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<211> 14

<212> PRT

<213> Bovine sp.

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<210> 49

<211> 9

<212> PRT

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<210> 50

<211> 11

<212> PRT

<213> Bovine sp.

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<210> 51

<211> 25

<212> PRT

<213> Bovine sp.

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<223> all "Xaa" amino acids are unidentified

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5

10

15

Ala Gly Met Phe Ala Ile Xaa Ala Asp

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25

<210> 52

<211> 21

<212> PRT

<213> Bovine sp.

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<223> all "Xaa" amino acids are unidentified

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10

15

Arg Pro Gly Xaa Leu

20

<210> 53

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<212> PRT

<213> Bovine sp.

<400> 53

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5

10

15

<210> 54
 <211> 11
 <212> PRT
 <213> Bovine sp.

<400> 54
 Ala Thr Asn Gly Pro Arg Tyr Val Val Val Gly
 1 5 10

<210> 55
 <211> 7
 <212> PRT
 <213> Bovine sp.

<400> 55
 Glu Ile Asp Gly Arg Leu Lys
 1 5

<210> 56
 <211> 14
 <212> PRT
 <213> Bovine sp.

<400> 56
 Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys
 1 5 10

<210> 57
 <211> 8
 <212> PRT
 <213> Bovine sp.

<400> 57
 Ile Leu Ala Gly Pro Ile Thr Lys
 1 5

<210> 58
 <211> 16
 <212> PRT
 <213> Bovine sp.

<220>
 <223> all "Xaa" amino acids are unidentified

<400> 58
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 1 5 10 15

<210> 59
 <211> 9
 <212> PRT

<213> Bovine sp.

<400> 59

Val Val Ser Ser Ser Leu Val Asp Lys
1 5

<210> 60

<211> 7

<212> PRT

<213> Bovine sp.

<400> 60

Ala Leu Gln Asp Tyr Arg Lys
1 5

<210> 61

<211> 7

<212> PRT

<213> Bovine sp.

<400> 61

Glu His Arg Glu Gln Leu Lys
1 5

<210> 62

<211> 12

<212> PRT

<213> Bovine sp.

<400> 62

Lys Leu Glu Ser Lys Leu Asp Tyr Lys Pro Val Arg
1 5 10

<210> 63

<211> 5

<212> PRT

<213> Bovine sp.

<400> 63

Leu Val Pro Thr Arg
1 5

<210> 64

<211> 11

<212> PRT

<213> Bovine sp.

<400> 64

Ala Lys Glu Glu Glu Ile Glu Ala Gln Ile Lys
1 5 10

<210> 65

<211> 10
 <212> PRT
 <213> Bovine sp.

<400> 65
 Ala Asn Tyr Glu Val Leu Glu Ser Gln Lys
 1 5 10

<210> 66
 <211> 11
 <212> PRT
 <213> Bovine sp.

<400> 66
 Val Glu Asp Ala Leu His Gln Leu His Ala Arg
 1 5 10

<210> 67
 <211> 8
 <212> PRT
 <213> Bovine sp.

<400> 67
 Asp Val Asp Leu Tyr Gln Val Arg
 1 5

<210> 68
 <211> 13
 <212> PRT
 <213> Bovine sp.

<400> 68
 Gln Ser Gln Gly Leu Ser Pro Ala Gln Ala Phe Ala Lys
 1 5 10

<210> 69
 <211> 21
 <212> PRT
 <213> Bovine sp.

<400> 69
 Ala Gly Ser Gln Ser Gly Gly Ser Pro Glu Ala Ser Gly Val Thr Val
 1 5 10 15
 Ser Asp Val Gln Glu
 20

<210> 70
 <211> 12
 <212> PRT
 <213> Bovine sp.

<220>

<223> all "Xaa" amino acids are unidentified

<400> 70

Gly Leu Leu Gly Xaa Asn Ile Ile Pro Leu Gln Arg
 1 5 10

<210> 71

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P1

<400> 71

ttgaagaatg atgcattagg aaccac

26

<210> 72

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P2

<400> 72

cactcgagtg gctggatttc aatttctcca gtag

34

<210> 73

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P3

<400> 73

gtcgagctag ccatctcctc ttcg

24

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P4

<400> 74

catgggagac aggttccgag acc

23

<210> 75

<211> 9

<212> PRT

<213> Homo sapiens

<400> 75

Lys Gly Ile Pro Ser Phe Trp Leu Thr
1 5

<210> 76

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 76

Lys Gly Ile Pro Glu Phe Trp Leu Thr
1 5

<210> 77

<211> 10

<212> PRT

<213> Homo sapiens

<400> 77

Asp Ser Phe Phe Asn Phe Phe Ala Pro Pro
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 78

Glu Ser Phe Phe Asn Phe Phe Ser Pro
1 5

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: consensus
sequence

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<223> all "Xaa" amino acids are unidentified

<400> 79

Glu Xaa Xaa Lys Glu Xaa Pro Glu Val Lys Xaa Glu Glu Lys
1 5 10

<210> 80

<211> 5

<212> PRT

<213> HIV-1

<400> 80
 Gly Arg Lys Lys Arg
 1 5

<210> 81
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 81
 Lys Lys Lys Arg Lys
 1 5

<210> 82
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: A1 Primer

<400> 82
 cctaaaaagt gtctaagtgc cagtt 25

<210> 83
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: A2 Primer

<400> 83
 tcagtgaag ggaaggtaga acac 24

<210> 84
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: P1 Primer

<400> 84
 taatgaattt catttttagga ggtcgg 26

<210> 85
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P2 Primer

<400> 85

atcttttggg aaagtaagat gagcc

25

<210> 86

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C1 Primer

<400> 86

ggagactcac ctgctaattgt t

21

<210> 87

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C4 Primer

<400> 87

ctcaaaagca gtctcttggc

20

<210> 88

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer A

<400> 88

atgggagata cagtagtgga gc

22

<210> 89

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer B

<400> 89

tcacatgatg ccgttggtga g

21

<210> 90

<211> 51

<212> DNA

<213> Homo sapiens

<400> 90
 tggatcaagc caatacaaga ttcttgtgaa attacgactg atagtggcat g 51

<210> 91
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 91
 tccatttggg aacaggagcg agtgcccctt tggatcaagc catacaagat tcttgtgatt 60
 tcggctgata gtggcatgat tgaaccagtg gtcaatgctg tgtccatcca tcaggtg 117

<210> 92
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer C1

<400> 92
 ctcagatcta tgggagatac agtagtggag c 31

<210> 93
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer C2

<400> 93
 tcgagatctt cacatgatgc cgttggtgag 30

<210> 94
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: P1 Primer

<400> 94
 gatttgtgct caataatcac tatctgaa 28

<210> 95
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P2 Primer

<400> 95

ggttactagg atcacaaagt atgaattctg gaa

33